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START SEQ ID NO:2

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M P A 3
9

START SEQ ID NO:3

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A	C	Y	C	H	H	K	H	L	C	C	S	S	S	Y	I	P	Q	S	R	43
GCA	TGT	TAC	TGC	CAC	CAC	AAA	CAT	CTC	TGT	TGT	TCC	TCA	TCG	TAC	ATT	CCT	CAG	AGT	CGA	129

L R Y T P H P A Y A T F C R P K E N W W 63
CTG AGA TAC ACA CCT CAT CCA GCA TAT GCT ACC TTT TGC AGG CCA AAG GAG AAC TGG TGG 189

Q Y T Q G R R Y A S T P Q K F Y L T P P 83
CAG TAC ACC CAA GGA AGG AGA TAT GCT TCC ACA CCA CAG AAA TTT TAC CTC ACA CCT CCA 249

Q	V	N	S	I	L	K	A	N	E	Y	S	F	K	V	P	E	F	D	G	103
CAA	GTC	AAT	AGC	ATC	CCT	AAA	GCT	AAT	GAA	TAC	AGT	TTC	AAA	GTG	CCA	GAA	TTT	GAC	GGC	309

K	N	V	S	S	I	L	G	F	D	S	N	Q	L	P	A	N	A	P	I	123
AAA	AAT	GTC	AGT	TCT	ATC	CTT	GGA	TTT	GAC	AGC	AAT	CAG	CTG	CCT	GCA	AAT	GCA	CCC	ATT	369

E	D	R	R	S	A	A	T	C	L	Q	T	R	G	M	L	L	G	V	F	143
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A V S L L P H E T L L E I E N A V E S G 183
GCT GTC TCT TTG TTA CCC CAT GAG ACT TTG CTA GAG ATT GAA AAT GCA GTG GAG AGC GGC 549

R A L L P I L Q W H K H P N D Y F S K E 203
CGG GCA CTG CTA CCC ATT CTC CAG TGG CAC AAG CAC CCC AAT GAT TAC TTT AGT AAG GAG 609

A S K L Y F N S L R T Y W Q E L I D L N 223
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V L R V A F S G A T A C V A H V D G V D 283
GTG CTT CGA GTG GCA TTT TCT GGA GCC ACT GCT TGT GTG GCC CAT GTG GAT GGT GTT GAC 849

L	H	V	A	N	T	G	D	S	R	A	M	L	G	V	Q	E	E	D	G	303
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Fig. 1A

[illegible]

S W S A V T L S N D H N A Q N E R E L E 323
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 R L K L E H P K S E A K S V V K Q D R L 343
 CGG CTG AAA TTG GAA CAT CCA AAG AGT GAG GCC AAG AGT GTC GTG AAA CAG GAT CGG CTG 1029

 L G L L M P F R A F G D V K F K W S I D 363
 CTT GGC TTG CTG ATG CCA TTT AGG GCA TTT GGA GAT GTA AAG TTC AAA TGG AGC ATT GAC 1089

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 F I P P N Y H T P P Y L T A E P E V T Y 403
 TTT ATT CCT CCT AAT TAT CAC ACA CCT CCT TAT CTC ACT GCT GAG CCA GAG GTA ACT TAC 1209

 H R L R P Q D K F L V L A T D G L W E T 423
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 M H R Q D V V R I V G E Y L T G M H H Q 443
 ATG CAT AGG CAG GAT GTG GTT AGG ATT GTG GGT GAG TAC CTA ACT GGC ATG CAT CAC CAA 1329

 Q P I A V G G Y K V T L G Q M H G L L T 463
 CAG CCA ATA GCT GTT GGT GGC TAC AAG GTG ACT CTG GGA CAG ATG CAT GGC CTT TTA ACA 1389

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 L S L P E E L A R M Y R D D I T I I V V 523
 CTT AGT CTT CCT GAA GAG CTT GCT CGA ATG TAC AGA GAT GAC ATT ACA ATC ATT GTA GTT 1569

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Fig. 1B

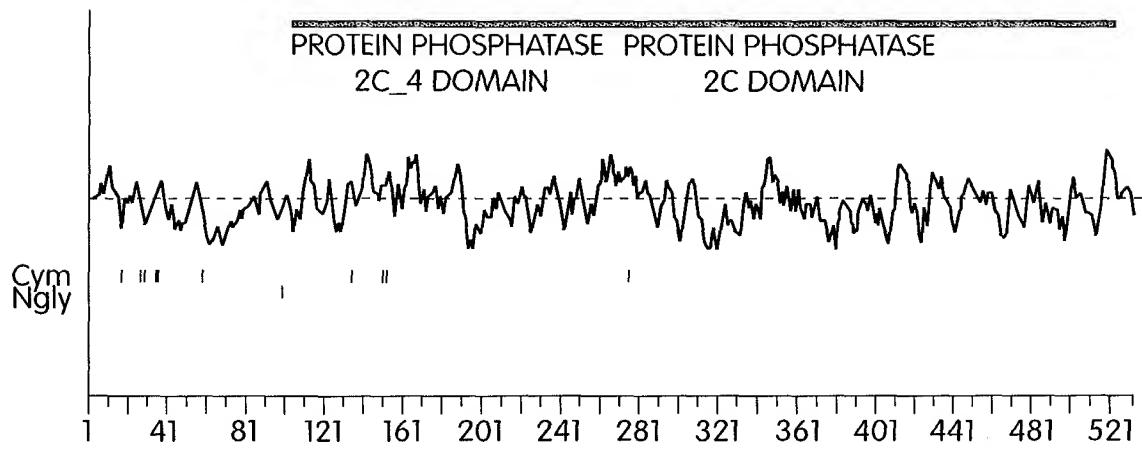


Fig. 2

PP2C: domain 1 of 1, from 173 to 461: score 261.3, E = 1.3e-74

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 26583 219 LIDLNTGESTDIdVKEALINAFKRLDN-----DISLEAQVGDPNsFLNY 262
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 26583 400 EVT-YHRLRPQ-DKFLVLATDGLWETMHRQDVVRIVGEYLTGM-----H 441
 meaaeklvdeaiargaeDni<-*
 ++ ++ + + g ++
 26583 442 HQQPIAVGGYKVTLGQMHGL 461

Fig. 3A

PP2C_4: domain 1 of 1, from 99 to 523: score 338.5, E = 7.6e-98

```

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      v
26583  523 V   523

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Fig. 3B

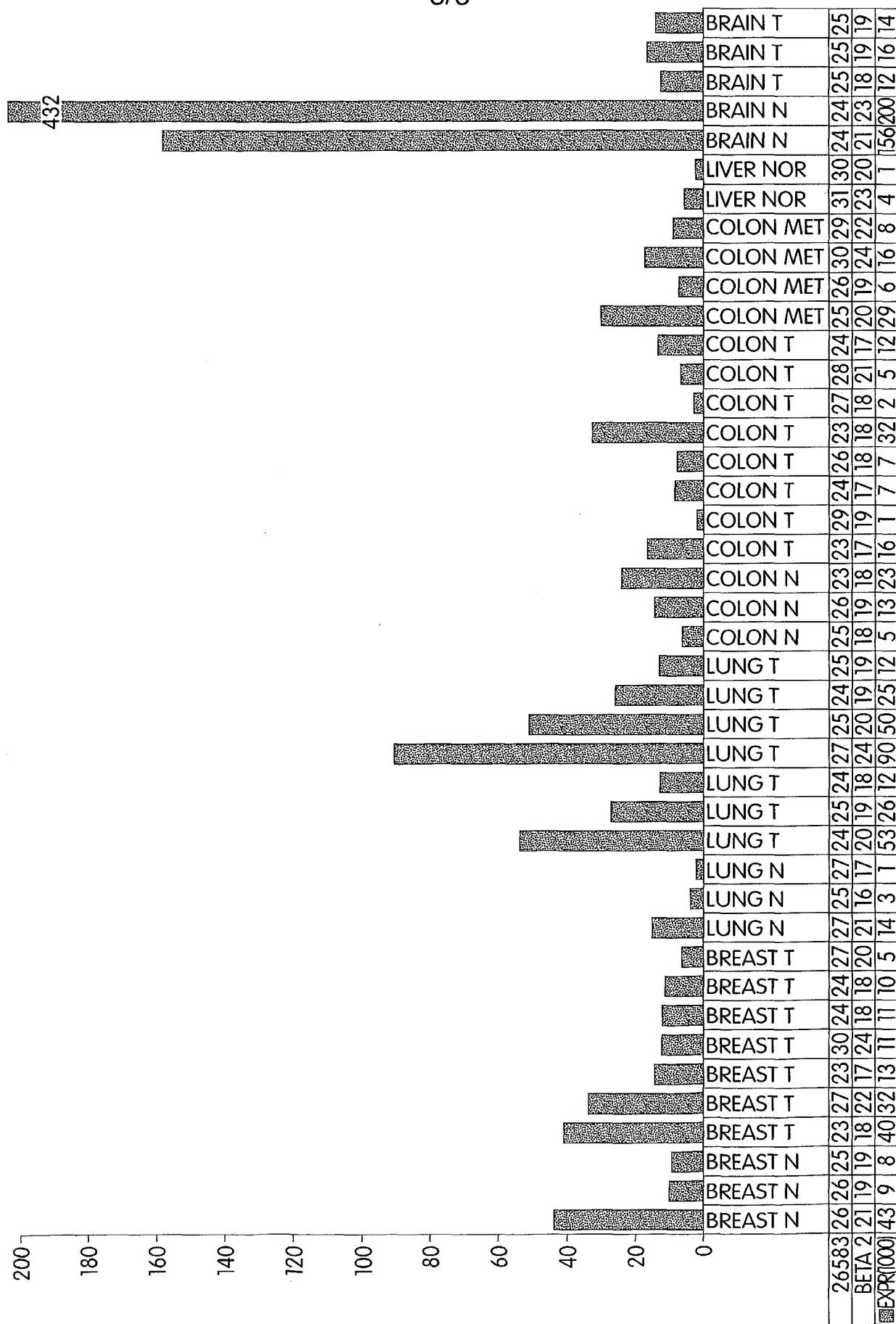


Fig. 4